Metagenome: differences in the gut microbiota among healthy, obese and type 2 diabetes adults

ABSTRACT

The association between gut microbiota composition with pathogenesis of metabolic diseases namely obesity and type 2 diabetes are increasingly recognized. The aim of the study was to identify the diversity of gut microbiota phylum and families in the gut of healthy, obese and type 2 diabetes adults with metagenomic approach. Six healthy subjects, five obese subjects and five type 2 diabetes subjects of similar inclusion and exclusion criteria were recruited. The different bacterial phyla and families in the stool sample were analyzed with metagenomic analysis. The median (IQR)% of relative abundance for each phylum and families were analyzed. The obese subjects had higher Bacteroidetes 63.50(21.55)% with lower Firmicutes 27.00(13.55)%, meanwhile, the type 2 diabetes subjects also had higher Bacteroidetes 66.50(39.00)% with lower Firmicutes 27.70(19.35)%. These findings shows that there are differences in the gut microbiota composition in the healthy, obese and type 2 diabetes adults which may influence the development of obesity and type 2 diabetes.

Keyword: Obese; Type 2 diabetes; Metagenome